

(A)

Wed Nov 21 09:18:30 2001 [BLASTN 2.2.1 [Jul-12-2001], NCBI]  
Repeats masked (summary below)  
/home/ruby/va/Molbio/carpanda/tempblast/ss.DNA59842 (1141 bp)

Sequences producing High-scoring Segment Pairs:		Frame	Score	Match
Pct	E-val			
1	P_AAC58384 Human PRO1153 nucleotide sequence SEQ ID	+	1141	1141
100	0.0			
2	P_AAZ65081 Membrane-bound protein PRO1153 encoding	+	1141	1141
100	0.0			
3	P_AAF44227 Human PRO1153 (UNQ583) nucleotide sequen	+	1141	1141
100	0.0			
4	BC009558 Homo sapiens, clone IMAGE:3899550, mRNA,	+	1137	1140
100	0.0			
5	P_AAD12571 Human protein having hydrophobic domain	+	1133	1136
100	0.0			
6	AX191504 Sequence 26 from Patent WO0149728. DNA,	+	1133	1136
100	0.0			

>1 P\_AAC58384 Human PRO1153 nucleotide sequence SEQ ID NO:48. (1141 bp)  
[1 seg]  
Score = 1141 (2262 bits), Expect = 0.0  
Identities = 1141/1141 (100%), at 1,1-1141,1141, Strand +/-

ss.DNA59842 1  
GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

\*\*\*\*\*  
P\_AAC58384 1  
GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842 61  
GGCCCCGACCCCGCCGCGCCGACCCCGCCGCGCCGACCCCGCCGCGCCGACCCCGCCGCGCCG

\*\*\*\*\*  
P\_AAC58384 61  
GGCCCCGACCCCGCCGCGCCGACCCCGCCGCGCCGACCCCGCCGCGCCGACCCCGCCGCGCCG

ss.DNA59842 121  
GCCGCTCACCAGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

\*\*\*\*\*  
P\_AAC58384 121  
GCCGCTCACCAGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842 181  
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

\*\*\*\*\*  
P\_AAC58384 181  
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842 241  
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

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P\_AAC58384 241  
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

BLAST RESULTS A-1

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ss.DNA59842 301
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P_AAC58384 301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC
*****
P_AAC58384 361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT
*****
P_AAC58384 421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

ss.DNA59842 481
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*****
P_AAC58384 481
TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842 541
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*****
P_AAC58384 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

ss.DNA59842 601
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*****
P_AAC58384 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

ss.DNA59842 661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCTTCAGTGAT
*****
P_AAC58384 661
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ss.DNA59842 721
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*****
P_AAC58384 721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

ss.DNA59842 781
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*****
P_AAC58384 781

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BLAST RESULTS A-2

CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

ss.DNA59842 841

AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTTGGGGGAGGGCTTGAATT

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P\_AAC58384 841

AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTTGGGGGAGGGCTTGAATT

ss.DNA59842 901

ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

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P\_AAC58384 901

ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

ss.DNA59842 961

TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

\*\*\*\*\*

P\_AAC58384 961

TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

ss.DNA59842 1021

CCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

\*\*\*\*\*

P\_AAC58384 1021

CCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081

CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

\*\*\*\*\*

P\_AAC58384 1081

CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

ss.DNA59842 1141 A

\*

P\_AAC58384 1141 A

>2 P\_AAZ65081 Membrane-bound protein PRO1153 encoding cDNA. (1141 bp) [1  
seg]

Score = 1141 (2262 bits), Expect = 0.0

Identities = 1141/1141 (100%), at 1,1-1141,1141, Strand +/+

ss.DNA59842 1

GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

\*\*\*\*\*

P\_AAZ65081 1

GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842 61

GGCCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC

\*\*\*\*\*

P\_AAZ65081 61

GGCCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC

ss.DNA59842 121

BLAST RESULTS A-3

BLAST RESULTS A-4

GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

\*\*\*\*\*

P\_AAZ65081 121  
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842 181  
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\*\*\*\*\*

P\_AAZ65081 181  
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842 241  
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

\*\*\*\*\*

P\_AAZ65081 241  
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

ss.DNA59842 301  
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

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P\_AAZ65081 301  
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361  
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

\*\*\*\*\*

P\_AAZ65081 361  
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421  
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGAT

\*\*\*\*\*

P\_AAZ65081 421  
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGAT

ss.DNA59842 481  
TCCAATGACAGGCATCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

\*\*\*\*\*

P\_AAZ65081 481  
TCCAATGACAGGCATCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842 541  
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

\*\*\*\*\*

P\_AAZ65081 541  
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

ss.DNA59842 601  
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

\*\*\*\*\*

P\_AAZ65081 601  
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

ss.DNA59842 661  
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

\*\*\*\*\*  
P\_AAZ65081 661  
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ss.DNA59842 721  
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P\_AAZ65081 721  
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ss.DNA59842 781  
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

\*\*\*\*\*  
P\_AAZ65081 781  
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

ss.DNA59842 841  
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGGAATT

\*\*\*\*\*  
P\_AAZ65081 841  
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ss.DNA59842 901  
ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

\*\*\*\*\*  
P\_AAZ65081 901  
ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

ss.DNA59842 961  
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\*\*\*\*\*  
P\_AAZ65081 961  
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ss.DNA59842 1021  
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\*\*\*\*\*  
P\_AAZ65081 1021  
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081  
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

\*\*\*\*\*  
P\_AAZ65081 1081  
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

ss.DNA59842 1141 A

P\_AAZ65081 1141 A

BLAST RESULTS A-5

BLAST RESULTS A-10

>3 P\_AAF44227 Human PRO1153 (UNQ583) nucleotide sequence SEQ ID NO:350.  
(1141 bp) [1 seg]  
Score = 1141 (2262 bits), Expect = 0.0  
Identities = 1141/1141 (100%), at 1,1-1141,1141, Strand +/+

ss.DNA59842 1  
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

\*\*\*\*\*  
P\_AAF44227 1  
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842 61  
GGCCCCGACCCCGGGCGCGCCAGCCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGC

\*\*\*\*\*  
P\_AAF44227 61  
GGCCCCGACCCCGGGCGCGCCAGCCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGC

ss.DNA59842 121  
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

\*\*\*\*\*  
P\_AAF44227 121  
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842 181  
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\*\*\*\*\*  
P\_AAF44227 181  
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ss.DNA59842 241  
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\*\*\*\*\*  
P\_AAF44227 241  
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ss.DNA59842 301  
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\*\*\*\*\*  
P\_AAF44227 301  
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361  
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\*\*\*\*\*  
P\_AAF44227 361  
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421  
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGAT

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P\_AAF44227 421  
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGAT

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ss.DNA59842 481
TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG
*****
P_AAF44227 481
TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842 541
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*****
P_AAF44227 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCC

ss.DNA59842 601
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P_AAF44227 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

ss.DNA59842 661
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*****
P_AAF44227 661
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ss.DNA59842 721
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*****
P_AAF44227 721
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ss.DNA59842 781
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*****
P_AAF44227 781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

ss.DNA59842 841
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGAATT
*****
P_AAF44227 841
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGAATT

ss.DNA59842 901
ATGGGCTATTTTTACTGGGGGCAAGGGAGGSAGATGACAGCCTGGGTACAGTGCCTGTT
*****
P_AAF44227 901
ATGGGCTATTTTTACTGGGGGCAAGGGAGGSAGATGACAGCCTGGGTACAGTGCCTGTT

ss.DNA59842 961
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P_AAF44227 961

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BLAST RESULTS A-7

BLAST RESULTS A-9

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TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT
ss.DNA59842 1021
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P_AAF44227 1021
CCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC
ss.DNA59842 1081
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA
*****
P_AAF44227 1081
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA
ss.DNA59842 1141 A
*
P_AAF44227 1141 A
>4 BC009558 Homo sapiens, clone IMAGE:3899550, mRNA, partial cds. (1156
bp) [1 seg]
Score = 1137 (2254 bits), Expect = 0.0
Identities = 1140/1141 (99%), at 1,5-1141,1145, Strand +/-
ss.DNA59842 1
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA
*****
BC009558 5
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA
ss.DNA59842 61
GGCCCCGACCCCGGCCGCGCCAGCCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC
*****
BC009558 65
GGCCCCGACCCCGGCCGCGCCAGCCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC
ss.DNA59842 121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA
*****
BC009558 125
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA
ss.DNA59842 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT
*****
BC009558 185
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT
ss.DNA59842 241
CACCTTCTGCTGCGGGACCTGCTACCATCGSTACTGCTGCAGGGACCTGACCTTGCTTAT
*****
BC009558 245
CACCTTCTGCTGCGGGACCTGCTACCATCGSTACTGCTGCAGGGACCTGACCTTGCTTAT
ss.DNA59842 301
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CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC  
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 BC009558 305  
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 ss.DNA59842 361  
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 \*\*\*\*\*  
 BC009558 365  
 CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC  
 ss.DNA59842 421  
 CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT  
 \*\*\*\*\*  
 BC009558 425  
 CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT  
 ss.DNA59842 481  
 TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG  
 \*\*\*\*\*  
 BC009558 485  
 TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG  
 ss.DNA59842 541  
 CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC  
 \*\*\*\*\*  
 BC009558 545  
 CCCTGCACCCCCACAGCCTGGCTTCATATACCCACCTAGTGGTCCTGCTCCCCAATATCC  
 ss.DNA59842 601  
 ACTCTACCCAGCTGGGCCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC  
 \*\*\*\*\*  
 BC009558 605  
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 ss.DNA59842 661  
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 \*\*\*\*\*  
 BC009558 665  
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 ss.DNA59842 721  
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 \*\*\*\*\*  
 BC009558 725  
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 ss.DNA59842 781  
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 BC009558 785  
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BLAST RESULTS A-9

ss.DNA59842 841  
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGGAATT

\*\*\*\*\*  
BC009558 845  
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ss.DNA59842 901  
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

\*\*\*\*\*  
BC009558 905  
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

ss.DNA59842 961  
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

\*\*\*\*\*  
BC009558 965  
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ss.DNA59842 1021  
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

\*\*\*\*\*  
BC009558 1025  
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081  
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\*\*\*\*\*  
BC009558 1085  
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ss.DNA59842 1141 A

\*  
BC009558 1145 A

>5 P\_AAD12571 Human protein having hydrophobic domain encoding cDNA  
clone HP10764. (1372 bp) [1 seg]  
Score = 1133 (2246 bits), Expect = 0.0  
Identities = 1136/1137 (99%), at 1,236-1137,1372, Strand +/-

ss.DNA59842 1  
GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

\*\*\*\*\*  
P\_AAD12571 236  
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ss.DNA59842 61  
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\*\*\*\*\*  
P\_AAD12571 296  
GGCCCCGACCCGCGCGCGCCAGCCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCG

ss.DNA59842 121  
GCCGCTCACCAGCAATCGCTCTGTTGGTGGTGGGGGCTCCCTGGTGCTGGCCGGCGAGGA

\*\*\*\*\*  
P\_AAD12571 356  
GCCGCTCACC3CAATCGCTCTGTTGGTGGTGGGGCTCCCCTGGTGGTGGCCGGCGAGGA

ss.DNA59842 181  
CTGCCTGTGGTACCTGGACCGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

\*\*\*\*\*  
P\_AAD12571 416  
CTGCCTGTGGTACCTGGACCGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842 241  
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

\*\*\*\*\*  
P\_AAD12571 476  
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

ss.DNA59842 301  
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

\*\*\*\*\*  
P\_AAD12571 536  
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361  
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

\*\*\*\*\*  
P\_AAD12571 596  
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421  
CTGTTGCTACCTGTACCGCGCGGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGAT

\*\*\*\*\*  
P\_AAD12571 656  
CTGTTGCTACCTGTACCGCGCGGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGAT

ss.DNA59842 481  
TCCAATGACAGGCATCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

\*\*\*\*\*  
P\_AAD12571 716  
TCCAATGACAGGCATCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842 541  
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC  
\*\*\*\*\*

\*\*\*\*\*  
P\_AAD12571 776  
CCCTGCACCCCCACAGCCTGGCTTCATATACCCACCTAGTGGTCCTGCTCCCCAATATCC

ss.DNA59842 601  
ACTCTACCCAGCTGGGCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

\*\*\*\*\*  
P\_AAD12571 836  
ACTCTACCCAGCTGGGCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

BLAST RESULTS A-11

ss.DNA59842 661  
ACAGCCCTCTTACCCGGGAGCCTGAGGAACGAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

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P\_AAD12571 896  
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ss.DNA59842 721  
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\*\*\*\*\*  
P\_AAD12571 956  
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ss.DNA59842 781  
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

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P\_AAD12571 1016  
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ss.DNA59842 841  
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\*\*\*\*\*  
P\_AAD12571 1076  
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGAATT

ss.DNA59842 901  
ATGGGCTATTTTTACTGGGGGAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

\*\*\*\*\*  
P\_AAD12571 1136  
ATGGGCTATTTTTACTGGGGGAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

ss.DNA59842 961  
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

\*\*\*\*\*  
P\_AAD12571 1196  
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

ss.DNA59842 1021  
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

\*\*\*\*\*  
P\_AAD12571 1256  
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081  
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

\*\*\*\*\*  
P\_AAD12571 1316  
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

>6 AX191504 Sequence 26 from Patent WO0149728. DNA, PAT 15-AUG-2001  
(1372 bp) [1 seg]  
Score = 1133 (2246 bits), Expect = 0.0  
Identities = 1136/1137 (99%), at 1,236-1137,1372, Strand +/-

BLAST RESULTS A-12

```

ss.DNA59842      1
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA
*****
AX191504      236
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842      61
GGCCCCGACCCCGGCGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCG
*****
AX191504      296
GGCCCCGACCCCGGCGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCG

ss.DNA59842      121
GCCGCTCACC GCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA
*****
AX191504      356
GCCGCTCACC GCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842      181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT
*****
AX191504      416
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842      241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT
*****
AX191504      476
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

ss.DNA59842      301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC
*****
AX191504      536
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842      361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC
*****
AX191504      596
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842      421
CTGTTGCTACCTGTACCGCGCGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT
*****
AX191504      656
CTGTTGCTACCTGTACCGCGCGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

ss.DNA59842      481
TCCAATGACAGGCATCCCAGTGCCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG
*****
AX191504      716

```

BLAST RESULTS A-13

TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG  
ss.DNA59842 541  
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC  
\*\*\*\*\*  
AX191504 776  
CCCTGCACCCCCACAGCCTGGCTTCATATACCCACCTAGTGGTCCTGCTCCCCAATATCC  
ss.DNA59842 601  
ACTCTACCCAGCTGGGCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC  
\*\*\*\*\*  
AX191504 836  
ACTCTACCCAGCTGGGCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC  
ss.DNA59842 661  
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGAT  
\*\*\*\*\*  
AX191504 896  
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGAT  
ss.DNA59842 721  
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT  
\*\*\*\*\*  
AX191504 956  
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT  
ss.DNA59842 781  
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC  
\*\*\*\*\*  
AX191504 1016  
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC  
ss.DNA59842 841  
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGAATT  
\*\*\*\*\*  
AX191504 1076  
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGAATT  
ss.DNA59842 901  
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT  
\*\*\*\*\*  
AX191504 1136  
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT  
ss.DNA59842 961  
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT  
\*\*\*\*\*  
AX191504 1196  
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT  
ss.DNA59842 1021  
CCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

## BLAST RESULTS A-H

\*\*\*\*\*  
AX191504 1256  
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGSCAGTAGCCCTC

ss.DNA59842 1081  
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

\*\*\*\*\*  
AX191504 1316  
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

BLAST RESULTS A-15

(B)

BLAST RESULTS B-1

Wed Nov 21 09:32:36 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]  
/home/ruby/va/Molbio/carpenda/tempblast/pl.DNA59842.nc (197 aa)

Sequences producing High-scoring Segment Pairs:			Score	Match	Pct	E-val
1	P_AAB65258	Human PRO1153 (UNQ583) protein sequence S	1118	197	100	e-121
2	P_AAG81325	Human AFP protein sequence SEQ ID NO:168	1118	197	100	e-121
3	P_AAY66735	Membrane-bound protein PRO1153 - Homo sap	1118	197	100	e-121
4	P_AAB24074	Human PRO1153 protein sequence SEQ ID NO:	1118	197	100	e-121
5	CAC38575.1	unnamed protein product - Homo sapiens	1118	197	100	e-121
6	P_AAE06576	Human protein having hydrophobic domain,	1114	196	99	e-121
7	CAC51150.1	unnamed protein product - Homo sapiens	1114	196	99	e-121

>1 P\_AAB65258 Human PRO1153 (UNQ583) protein sequence SEQ ID NO:351 - Homo (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121

Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAB65258       1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR

DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCF LCSCCYLYRRRQQ
                  *****
P_AAB65258      61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCF LCSCCYLYRRRQQ

DNA59842.nc     121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAB65258      121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc     181 PAAPPPYMPPQPSYPGA
                  *****
P_AAB65258      181 PAAPPPYMPPQPSYPGA
```

>2 P\_AAG81325 Human AFP protein sequence SEQ ID NO:168 - Homo sapiens. (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121

Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAG81325       1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR

DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCF LCSCCYLYRRRQQ
                  *****
P_AAG81325      61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCF LCSCCYLYRRRQQ

DNA59842.nc     121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAG81325      121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc     181 PAAPPPYMPPQPSYPGA
                  *****
P_AAG81325      181 PAAPPPYMPPQPSYPGA
```

>3 P\_AAY66735 Membrane-bound protein PRO1153 - Homo sapiens. (197 aa) [1 seg]



Score = 1118 (435 bits), Expect = e-121  
Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAY66735      1 MPPAGLRRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
P_AAY66735     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAY66735    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
DNA59842.nc    181 PAAPPPYMPQPQPSYPGA
                  *****
P_AAY66735    181 PAAPPPYMPQPQPSYPGA
                  *****
```

>4 P\_AAB24074 Human PRO1153 protein sequence SEQ ID NO:49 - Homo sapiens. (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121  
Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAB24074      1 MPPAGLRRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
P_AAB24074     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAB24074    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
DNA59842.nc    181 PAAPPPYMPQPQPSYPGA
                  *****
P_AAB24074    181 PAAPPPYMPQPQPSYPGA
                  *****
```

>5 CAC38575.1 unnamed protein product - Homo sapiens (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121  
Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
CAC38575.1      1 MPPAGLRRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
CAC38575.1     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
CAC38575.1    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
DNA59842.nc    181 PAAPPPYMPQPQPSYPGA
                  *****
```

BLAST RESULTS B-2

CAC38575.1 181 PAAPPPYMPPQPSYPGA

>6 P\_AAE06576 Human protein having hydrophobic domain, HP10764 - Homo (197 aa) [1 seg]

Score = 1114 (433 bits), Expect = e-121

Identities = 196/197 (99%), Positives = 197/197 (99%), at 1,1-197,197

DNA59842.nc 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR  
\*\*\*\*\*

P\_AAE06576 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR

DNA59842.nc 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ  
\*\*\*\*\*

P\_AAE06576 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

DNA59842.nc 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYN  
\*\*\*\*\*

P\_AAE06576 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFIYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc 181 PAAPPPYMPPQPSYPGA  
\*\*\*\*\*

P\_AAE06576 181 PAAPPPYMPPQPSYPGA

>7 CAC51150.1 unnamed protein product - Homo sapiens (197 aa) [1 seg]

Score = 1114 (433 bits), Expect = e-121

Identities = 196/197 (99%), Positives = 197/197 (99%), at 1,1-197,197

DNA59842.nc 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR  
\*\*\*\*\*

CAC51150.1 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR

DNA59842.nc 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ  
\*\*\*\*\*

CAC51150.1 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

DNA59842.nc 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYN  
\*\*\*\*\*

CAC51150.1 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFIYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc 181 PAAPPPYMPPQPSYPGA  
\*\*\*\*\*

CAC51150.1 181 PAAPPPYMPPQPSYPGA